



SEQUENCE LISTING

<110> JENSEN, Ma in Roland et al.  
<120> NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID  
<130> 3631-0107P  
<140> 09/785,215  
<141> 2001-02-20  
  
<160> 19  
  
<170> PatentIn version 3.1

<210> 1  
<211> 2313  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(2313)  
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<220>  
<221> misc\_feature  
<222> (2098)..(2169)  
<223> nucleotides encoding transmembrane region

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<222> (2014)..(2313)  
<223> Nucleotides encoding C-100

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<222> (2016)..(2144)  
<223> Abeta 42/43

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<223> Abeta 42/43

<400> 1  
atg ctg ccc ggt ttg gca ctg ctc ctg ctg gcc gcc tgg acg gct cgg  
Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg  
1 5 10 15

48

gcg ctg gag gta ccc act gat ggt aat gct ggc ctg ctg gct gaa ccc Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro 20 25 30	96
cag att gcc atg ttc tgt ggc aga ctg aac atg cac atg aat gtc cag Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln 35 40 45	144
aat ggg aag tgg gat tca gat cca tca ggg acc aaa acc tgc att gat Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp 50 55 60	192
acc aag gaa ggc atc ctg cag tat tgc caa gaa gtc tac cct gaa ctg Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu 65 70 75 80	240
cag atc acc aat gtg gta gaa gcc aac caa cca gtg acc atc cag aac Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn 85 90 95	288
tgg tgc aag cgg ggc cgc aag cag tgc aag acc cat ccc cac ttt gtg Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val 100 105 110	336
att ccc tac cgc tgc tta gtt ggt gag ttt gta agt gat gcc ctt ctc Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu 115 120 125	384
gtt cct gac aag tgc aaa ttc tta cac cag gag agg atg gat gtt tgc Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys 130 135 140	432
gaa act cat ctt cac tgg cac acc gtc gcc aaa gag aca tgc agt gag Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu 145 150 155 160	480
aag agt acc aac ttg cat gac tac ggc atg ttg ctg ccc tgc gga att Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile 165 170 175	528
gac aag ttc cga ggg gta gag ttt gtg tgt tgc cca ctg gct gaa gaa Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu 180 185 190	576
agt gac aat gtg gat tct gct gat gcg gag gag gat gac tcg gat gtc Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val 195 200 205	624
tgg tgg ggc gga gca gac aca gac tat gca gat ggg agt gaa gac aaa Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys 210 215 220	672
gta gta gaa gta gca gag gag gaa gaa gtg gct gag gtg gaa gaa gaa Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu 225 230 235 240	720

gaa gcc gat gat gac gag gac gat gag gat ggt gat gag gta gag gaa Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu 245 250 255	768
gag gct gag gaa ccc tac gaa gaa gcc aca gag aga acc acc agc att Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile 260 265 270	816
gcc acc acc acc acc acc acc acc aca gag tct gtg gaa gag gtg gtt cga Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg 275 280 285	864
gag gtg tgc tct gaa caa gcc gag acg ggg ccg tgc cga gca atg atc Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile 290 295 300	912
tcc cgc tgg tac ttt gat gtg act gaa ggg aag tgt gcc cca ttc ttt Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe 305 310 315 320	960
tac ggc gga tgt ggc ggc aac cgg aac aac ttt gac aca gaa gag tac Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr 325 330 335	1008
tgc atg gcc gtg tgt ggc agc gcc atg tcc caa agt tta ctc aag act Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr 340 345 350	1056
acc cag gaa cct ctt gcc cga gat cct gtt aaa ctt cct aca aca gca Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala 355 360 365	1104
gcc agt acc cct gat gcc gtt gac aag tat ctc gag aca cct ggg gat Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp 370 375 380	1152
gag aat gaa cat gcc cat ttc cag aaa gcc aaa gag agg ctt gag gcc Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala 385 390 395 400	1200
aag cac cga gag aga atg tcc cag gtc atg aga gaa tgg gaa gag gca Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala 405 410 415	1248
gaa cgt caa gca aag aac ttg cct aaa gct gat aag aag gca gtt atc Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile 420 425 430	1296
cag cat ttc cag gag aaa gtg gaa tct ttg gaa cag gaa gca gcc aac Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn 435 440 445	1344
gag aga cag cag ctg gtg gag aca cac atg gcc aga gtg gaa gcc atg Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met 450 455 460	1392

ctc aat gac cgc cgc cgc ctg gcc ctg gag aac tac atc acc gct ctg	1440
Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu	
465 470 475 480	
cag gct gtt cct cct cgg cct cgt cac gtg ttc aat atg cta aag aag	1488
Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys	
485 490 495	
tat gtc cgc gca gaa cag aag gac aga cag cac acc cta aag cat ttc	1536
Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe	
500 505 510	
gag cat gtg cgc atg gtg gat ccc aag aaa gcc gct cag atc cgg tcc	1584
Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser	
515 520 525	
cag gtt atg aca cac ctc cgt gtg att tat gag cgc atg aat cag tct	1632
Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser	
530 535 540	
ctc tcc ctg ctc tac aac gtg cct gca gtg gcc gag gag att cag gat	1680
Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp	
545 550 555 560	
gaa gtt gat gag ctg ctt cag aaa gag caa aac tat tca gat gac gtc	1728
Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val	
565 570 575	
ttg gcc aac atg att agt gaa cca agg atc agt tac gga aac gat gct	1776
Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala	
580 585 590	
ctc atg cca tct ttg acc gaa acg aaa acc acc gtg gag ctc ctt ccc	1824
Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro	
595 600 605	
gtg aat gga gag ttc agc ctg gac gat ctc cag ccg tgg cat tct ttt	1872
Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe	
610 615 620	
ggg gct gac tct gtg cca gcc aac aca gaa aac gaa gtt gag cct gtt	1920
Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val	
625 630 635 640	
gat gcc cgc cct gct gcc gac cga gga ctg acc act cga cca ggt tct	1968
Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser	
645 650 655	
ggg ttg aca aat atc aag acg gag gag atc tct gaa gtg aag atg gat	2016
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp	
660 665 670	
gca gaa ttc cga cat gac tca gga tat gaa gtt cat cat caa aaa ttg	2064
Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu	
675 680 685	

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gtg ttc ttt gca gaa gat gtg ggt tca aac aaa ggt gca atc att gga 2112  
Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

ctc atg gtg ggc ggt gtt gtc ata gcg aca gtg atc gtc atc acc ttg 2160  
Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
705 710 715 720

gtg atg ctg aag aag aaa cag tac aca tcc att cat cat ggt gtg gtg 2208  
Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

gag gtt gac gcc gct gtc acc cca gag gag cgc cac ctg tcc aag atg 2256  
Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
740 745 750

cag cag aac ggc tac gaa aat cca acc tac aag ttc ttt gag cag atg 2304  
Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met  
755 760 765

cag aac tag 2313  
Gln Asn  
770

<210> 2  
<211> 770  
<212> PRT  
<213> Homo sapiens

<400> 2

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg  
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

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Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr	325	330	335
Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr	340	345	350
Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala	355	360	365
Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	370	375	380
Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala	385	390	395
Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala	405	410	415
Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile	420	425	430
Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn	435	440	445
Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met	450	455	460
Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu	465	470	475
Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys	485	490	495
Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe	500	505	510
Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser	515	520	525
Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	Arg	Met	Asn	Gln	Ser	530	535	540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met  
755 760 765



Gln Asn  
770

<210> 3  
<211> 45  
<212> DNA  
<213> Clostridium tetani  
  
<220>  
<221> CDS  
<222> (1)..(45)  
<223> DNA encoding P2 epitope

<400> 3  
cag tac atc aaa gct aac tcc aaa ttc atc ggt atc acc gag ctg 45  
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
1 5 10 15

<210> 4  
<211> 15  
<212> PRT  
<213> Clostridium tetani

<400> 4  
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu  
1 5 10 15

<210> 5  
<211> 63  
<212> DNA  
<213> Clostridium tetani

<220>  
<221> CDS  
<222> (1)..(63)  
<223> DNA encoding P30 epitope

<400> 5  
ttc aac aac ttc acc gta agc ttc tgg ctg cgt gtt ccg aaa gtt agc 48  
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
1 5 10 15

gct agc cac ctg gaa 63  
Ala Ser His Leu Glu  
20

<210> 6  
<211> 21

<212> PRT  
 <213> Clostridium tetani  
 <400> 6

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
 1 5 10 15

Ala Ser His Leu Glu  
 20

<210> 7  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer targeted to the pAB1 plasmid

<400> 7  
 caactcagct tcctttcggg c 21

<210> 8  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer targeted to the pAB1 plasmid

<400> 8  
 agatctcgat cccgcgaaat t 21

<210> 9  
 <211> 135  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer that encodes the human abeta-43 fragment with E. coli  
 optimised codons

<400> 9  
 atggatgcag aattccgtca cgactccggt tacgaagttc accaccagaa actgggttttc 60  
 ttgcgagaag atgttggttc caacaaaggt gcaatcatcg gtctgatggt tggcgggtgtt 120  
 gttatcgcga cctag 135

<210> 10  
 <211> 31

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer derived from SEQ ID NO:9

<400> 10  
gccggccatg gatgcagaat tccgtcacga c 31

<210> 11  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer derived from SEQ ID NO:9

<400> 11  
gccggaagct tctaggtcgc gataacaaca ccgccaacc 39

<210> 12  
<211> 84  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer encoding the P2 epitope

<400> 12  
ccggcaagct tctacagctc ggtgataccg atgaatttgg agttagcttt gatgtactgg 60  
gtcgcgataa caacaccgcc aacc 84

<210> 13  
<211> 101  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer derived from the pAB1 plasmid

<400> 13  
gccggccatg ggtttcaaca acttcaccgt tagcttctgg ctgcgtgttc cgaaagttag 60  
cgcgagccac ctggaagatg cagaattccg tcacgactcc g 101

<210> 14  
<211> 172  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Primer derived from the pAB2 plasmid

<400> 14  
 gggccaagct tggatccggt cgcgataaca acaccgcaa ccatcagacc gatgattgca 60  
 cctttgttgg aaccaacatc ttctgcgaag aaaaccagtt tctggtggtg aacttcgtaa 120  
 ccggagtcgt gacggaactc tgcattcagc tcggtgatac cgatgaattt gg 172

<210> 15  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer derived from the pAB3 plasmid

<400> 15  
 ctggaagatg cagagttccg tcacgactcc 30

<210> 16  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer derived from the pAB3 plasmid

<400> 16  
 gcgcgggata cttcaacaac ttcaccgtta gcttc 35

<210> 17  
 <211> 8  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificial sequence, used as an example for how to calculate  
 sequence identity, has 75% sequence identity with SEQ ID NO:18

<400> 17  
 agtcagtc 8

<210> 18  
 <211> 8  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificial sequence, used as an example for how to calculate  
 sequence identity, has 75% sequence identity with SEQ ID NO:17

<400> 18  
aatcaatc

8

<210> 19  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> artificial T-cell epitope capable of binding to a large portion  
of MHC Class II molecules in a variety of animals

<400> 19

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala  
1 5 10

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